What is claimed is:

1. A method for improving the nutritional value of a phytate-containing foodstuff comprising:
contacting said phytate-containing foodstuff with a substantially pure phytase enzyme having an amino acid sequence of SEQ ID NO:2, such that said substantially pure phytase enzyme catalyzes the liberation of inorganic phosphate from the phytate in said phytate-containing foodstuff.

2. The method of claim 1, wherein said substantially pure phytase enzyme is produced by a recombinant expression system comprising a phytase-encoding nucleic acid having a nucleotide sequence selected from the group consisting of:

a) SEQ ID NO:1, and

b) SEQ ID NO:1 wherein T can also be U;

wherein the expression of the phytase-encoding nucleic acid leads to the production of said substantially pure phytase enzyme.

3. The method of claim 1, wherein the liberation of the inorganic phosphate from the phytate in said phytate-containing foodstuff occurs prior to the ingestion of said phytate-containing foodstuff by a recipient organism.

4. The method of claim 1, wherein the liberation of the inorganic phosphate from the phytate in said phytate-containing foodstuff occurs after the ingestion of said phytate-containing foodstuff by a recipient organism.

5. The method of claim 1, wherein the liberation of the inorganic phosphate from the phytate in said phytate-containing foodstuff occurs in part prior to and in part after the ingestion of said phytate-containing foodstuff by a recipient organism.

6. A recombinant expression system for use in the method of claim 2, wherein said recombinant expression system is contained in a host cell and expresses a nucleotide sequence encoding a phytase enzyme having an amino acid sequence as set forth in SEQ ID NO:2, and wherein the nucleotide sequence encoding said enzyme is operably linked to a transcription control sequence operable in said host cell.

7. A vector which comprises the expression system according to claim 6.

8. The expression system of claim 6, wherein the control sequence comprises a constitutive promoter.

9. The expression system of claim 6, wherein the control sequence comprises a tissue-specific promoter.

10. The expression system of claim 6, wherein said host cell is a prokaryotic cell.

11. The expression system of claim 6, wherein said host cell is a eukaryotic cell.

12. The expression system of claim 6, wherein said host cell is a plant cell.

13. The expression system of claim 6, wherein said nucleotide sequence is preceded by a polynucleotide sequence encoding a signal peptide operably linked to said nucleotide sequence.

14. The expression system of claim 13, wherein said signal peptide is the PR protein PR-S signal peptide from tobacco.

15. A prokaryotic cell modified to contain the expression system of claim 6.

16. A eukaryotic cell modified to contain the expression system of claim 6.

17. A plant cell, plant part or plant modified to contain the expression system of claim 6.

18. A method to produce an animal feed containing a microbial phytase comprising:

a) culturing the plant cell, plant part or plant of claim 17 under conditions wherein said nucleotide sequence is expressed; and

b) converting said plant cells, plant parts or plants into a composition suitable for animal feed.

19. A feed composition for animals which comprises the plant seeds, plant cells, plant parts or plants of claim 17 in admixture with a phytate-containing foodstuff.

20. A method to treat a human or an animal able to benefit from digestive enhancement by the activity of an exogenous phytase enzyme, which method comprises administering to said human or animal an amount of plant seeds, plant cells, plant parts or plants of a transgenic plant, wherein said transgenic plant is modified to contain an expression system which expresses a nucleotide sequence encoding a phytase enzyme in an amount effective to provide phytase activity in said human's or animal's digestive tract.

21. A transgenic non-human organism whose genome comprises a heterologous nucleic acid sequence encoding a polypeptide having phytase activity, wherein said transgene results in expression of a phytase polypeptide.

22. A method of generating a variant comprising:

obtaining a nucleic acid comprising a sequence as set forth in SEQ ID NO: 1, sequences substantially identical thereto, sequences complementary thereto, fragments comprising at least 30 consecutive nucleotides thereof, and fragments comprising at least 30 consecutive nucleotides of the sequences complementary to SEQ ID NO:1; and

modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence.

23. The method of claim 22, wherein the modifications are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, ligation reassembly, GSSM and any combination thereof.

24. The method of claim 22, wherein the modifications are introduced by error-prone PCR.

25. The method of claim 22, wherein the modifications are introduced by shuffling.

26. The method of claim 22, wherein the modifications are introduced by oligonucleotide-directed mutagenesis.

27. The method of claim 22, wherein the modifications are introduced by assembly PCR.

28. The method of claim 22, wherein the modifications are introduced by sexual PCR mutagenesis.

29. The method of claim 22, wherein the modifications are introduced by *in vivo* mutagenesis.

30. The method of claim 22, wherein the modifications are introduced by cassette mutagenesis.

31. The method of claim 22, wherein the modifications are introduced by recursive ensemble mutagenesis.

32. The method of claim 22, wherein the modifications are introduced by exponential ensemble mutagenesis.

33. The method of claim 22, wherein the modifications are introduced by site-specific mutagenesis.

34. A computer readable medium having stored thereon a nucleic acid sequence as set forth in SEQ ID NO:1, and sequences substantially identical thereto, or a polypeptide sequence as set forth in SEQ ID NO:2, and sequences substantially identical thereto.

35. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a nucleic acid sequence as set forth in SEQ ID NO:1, and sequences substantially identical thereto, or a polypeptide sequence as set forth in SEQ ID NO:2 and sequences substantially identical thereto.

36. The computer system of claim 35, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

37. The computer system of claim 36, wherein the sequence comparison algorithm comprises a computer program which indicates polymorphisms.

38. The computer system of claim 35, further comprising an identifier which identifies features in said sequence.

39. A method for comparing a first sequence to a reference sequence or a database of sequences wherein said first sequence is a nucleic acid sequence as set forth in SEQ ID NO:1, and sequences substantially identical thereto, or a polypeptide sequence as set forth in SEQ ID NO:2, and sequences substantially identical thereto comprising:

reading the first sequence and the reference sequence or database of sequences through use of a computer program which compares sequences; and

determining differences between the first sequence and the reference sequence or database of sequences with the computer program.

40. The method of claim 39, wherein determining differences between the first sequence and the reference sequence comprises identifying polymorphisms.

41. An isolated polynucleotide encoding a phytase enzyme having an amino acid sequence as set forth in SEQ ID NO:8, and having one or more amino acid modifications selected from W68E, Q84W, A95P, K97C, S168E, R180Y, N226C, Y277D or any combination thereof.

42. An isolated polynucleotide, or an oligonucleotide portion thereof, comprising a contiguous sequence of at least about ten nucleotides substantially identical to a nucleotide sequence of SEQ ID NO:7 or to a nucleotide sequence complementary thereto, the contiguous nucleotide sequence comprising nucleotide changes wherein at least nucleotide 390 is G; 391 is A; nucleotide 438 is T; 439 is G; 440 is G; 471 is C; 473 is T; 477 is T; 448 is G; 449 is T; 690 is G; 691 is A; 692 is G; 729 is T; 730 is A; 731 is T; 864 is T; 865 is G; 1017 is G or any combination thereof.

43. The polynucleotide of claim 41, wherein the polynucleotide has a nucleotide sequence 90% homologous to a sequence as set forth in SEQ ID NO:9.

44. The polynucleotide of claim 41, wherein the polynucleotide has a nucleotide sequence as set forth in SEQ ID NO:9.

45. An isolated polynucleotide comprising a nucleotide sequence substantially identical to SEQ ID NO:7, and wherein nucleotide 390 is G; 391 is A; nucleotide 438 is T; 439 is G; 440 is G; 471 is C; 473 is T; 477 is T; 448 is G; 449 is T; 690 is G; 691 is A; 692 is G; 729 is T; 730 is A; 731 is T; 864 is T; 865 is G; 1017 is G, or any combination thereof.

46. The polynucleotide of claim 45, comprising a nucleotide sequence substantially identical to SEQ ID NO:7, and having a modified nucleotide sequence selected from nucleotide 390 is G and 391 is A; nucleotide 438 is T, 439 is G and 440 is G; 471 is C and 473 is T; 477 is T, 448 is G, and 449 is T; 690 is G, 691 is A and 692 is G; 729 is T, 730 is A, and 731 is T; 864 is T and 865 is G; 1017 is G, or any combination thereof.

47. An expression vector containing a polynucleotide of any of claims 41,4 4, or 46.

48. The vector of claim 47, wherein the vector is a viral vector.

49. The vector of claim 47, wherein the vector is a bacterial vector.

50. A host cell containing a vector of claim 47.

51. The host cell of claim 50, wherein the cell is a prokaryotic cell.

52. The host cell of claim 51, wherein the cell is E. coli, P. pastoris, or S. pombe.

53. The host cell of claim 50, wherein the cell is a eukaryotic cell.

54. A substantially purified polypeptide having an amino acid sequence substantially identical to SEQ ID NO:8 and having one or more amino acid modifications selected from W68E, Q84W, A95P, K97C, S168E, R180Y, N226C, Y277D or any combination thereof, wherein the polypeptide has phytase activity.

55. The polypeptide of claim 54, wherein the polypeptide activity is tolerant to temperatures of at least 60 degrees C.

56. The polypeptide of claim 54, wherein the polypeptide activity is tolerant to temperatures of at least 70 degrees C.

57. The polypeptide of claim 54, wherein the polypeptide activity is tolerant to temperatures of at least 80 degrees C.

58. The polypeptide of claim 54, wherein the polypeptide has a half-life in gastric fluid at least about 2-fold greater than the corresponding wild-type polypeptide.

59. A substantially purified polypeptide having an amino acid sequence as set forth in SEQ ID NO:10.

60. A method for improving the nutritional value of a phytate-containing foodstuff comprising:
contacting said phytate-containing foodstuff with a substantially pure phytase enzyme having an amino acid sequence of a polypeptide of claim 15, such that said substantially pure phytase enzyme catalyzes the liberation of inorganic phosphate from the phytate in said phytate-containing foodstuff.

61. The method of claim 60, wherein said substantially pure phytase enzyme is produced by a recombinant expression system comprising a phytase-encoding nucleic acid having a nucleotide sequence selected from the group consisting of:

a) SEQ ID NO:9;

b) SEQ ID NO:9 wherein T can also be U;

wherein the expression of the phytase-encoding nucleic acid leads to the production of said substantially pure phytase enzyme; and

c) SEQ ID NO:7, wherein 390 is G; 391 is A; nucleotide 438 is T; 439 is G; 440 is G; 471 is C; 473 is T; 477 is T; 448 is G; 449 is T; 690 is G; 691 is A; 692 is G; 729 is T; 730 is A; 731 is T; 864 is T; 865 is G; 1017 is G, or any combination thereof.

62. The method of claim 60, wherein the liberation of the inorganic phosphate from the phytate in said phytate-containing foodstuff occurs prior to the ingestion of said phytate-containing foodstuff by a recipient organism.

63. The method of claim 60, wherein the liberation of the inorganic phosphate from the phytate in said phytate-containing foodstuff occurs after the ingestion of said phytate-containing foodstuff by a recipient organism.

64. The method of claim 60, wherein the liberation of the inorganic phosphate from the phytate in said phytate-containing foodstuff occurs in part prior to and in part after the ingestion of said phytate-containing foodstuff by a recipient organism.

65. A recombinant expression system for use in the method of claim 61, wherein said recombinant expression system is contained in a host cell and expresses a nucleotide sequence encoding a phytase enzyme having an amino acid sequence as set forth in SEQ ID NO:9, and wherein the nucleotide sequence encoding said enzyme is operably linked to a transcription control sequence operable in said host cell.

66. A vector which comprises the expression system according to claim 65.

67. The expression system of claim 65, wherein the control sequence comprises a constitutive promoter.

68. The expression system of claim 65, wherein the control sequence comprises a tissue-specific promoter.

69. The expression system of claim 65, wherein said host cell is a prokaryotic cell.

70. The expression system of claim 65, wherein said host cell is a eukaryotic cell.

71. The expression system of claim 65, wherein said host cell is a plant cell.

72. The expression system of claim 65, wherein said nucleotide sequence is preceded by a polynucleotide sequence encoding a signal peptide operably linked to said nucleotide sequence.

73. The expression system of claim 72, wherein said signal peptide is the PR protein PR-S signal peptide from tobacco.

74. A prokaryotic cell modified to contain the expression system of claim 65.

75. A eukaryotic cell modified to contain the expression system of claim 65.

76. A plant cell, plant part or plant modified to contain the expression system of claim 65.

77. A method to produce an animal feed containing a microbial phytase comprising:

a) culturing the plant cell, plant part or plant of claim 76 under conditions wherein said nucleotide sequence is expressed; and

b) converting said plant cells, plant parts or plants into a composition suitable for animal feed.

78. A feed composition for animals which comprises the plant seeds, plant cells, plant parts or plants of claim 76 in admixture with a phytate-containing foodstuff.

79. A method of generating a variant comprising:

obtaining a nucleic acid comprising a sequence as set forth in SEQ ID NO:9, sequences substantially identical thereto, sequences complementary thereto, fragments comprising at least 30 consecutive nucleotides thereof, and fragments comprising at least 30 consecutive nucleotides of the sequences complementary to SEQ ID NO:9; and

modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence.

80. The method of claim 79, wherein the modifications are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, ligation reassembly, GSSM and any combination thereof.

81. The method of claim 79, wherein the modifications are introduced by error-prone PCR.

82. The method of claim 79, wherein the modifications are introduced by shuffling.

83. The method of claim 79, wherein the modifications are introduced by oligonucleotide-directed mutagenesis.

84. The method of claim 79, wherein the modifications are introduced by assembly PCR.

85. The method of claim 79, wherein the modifications are introduced by sexual PCR mutagenesis.

86. The method of claim 79, wherein the modifications are introduced by *in vivo* mutagenesis.

87. The method of claim 79, wherein the modifications are introduced by cassette mutagenesis.

88. The method of claim 79, wherein the modifications are introduced by recursive ensemble mutagenesis.

89. The method of claim 79, wherein the modifications are introduced by exponential ensemble mutagenesis.

90. The method of claim 79, wherein the modifications are introduced by site-specific mutagenesis.